

Db 1741 CAAAAAAAAAAAA 1753

RESULT 4
AK024798
LOCUS AK024798 1577 bp mRNA linear PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ21145 fis, clone CAS08741.
ACCESSION AK024798
VERSION AK024798.1 GI:10437188
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens primary smooth muscle cells of human coronary artery
cDNA to mRNA, clone_lib:CAS clone:CAS08741.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 1577)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5' & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
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/organism="Homo sapiens"
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/cell_type="primary smooth muscle cells of human coronary
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/note="cloning vector pME18SFL3"
CDS 69. 1169
/note="unnamed protein product"
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LVADGCCNLQKQIQITQLFGVPVVALNVFKTDTRAIEDLVCELAKRAGAFDAVPCYH
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QAKIDRYTQGGFCNLPICMAKTHLSLHQDPDKGVPRDFILPISDVRSIGAGFIYPL
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BASE COUNT 424 a 336 c 420 g 397 t
ORIGIN

Query Match 42.8%; Score 1565.6; DB 9; Length 1577;
Best Local Similarity 99.7%; Pred. No. 1.9e-274;
Matches 1568; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2086 ggcagggaacacagagaaggccattaccggcaggcgagtttgacatcgagtgccca 2145
Db 1 GGCAGGGAACACAGAGAAGGCCATTACCGGCAGGCGAGTTTGACATCGCAGTGGCCA 60
Qy 2146 gcgagatcatggcggtgctggccctgacggacagcctcgagacatgaaggcagcgctgg 2205
Db 61 GCGAGATCATGGCGGTGCTGGCCCTGACGGACAGCCTCGCAGACATGAAGGCACGGCTGG 120

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OY	2266	tgaacagtgcttttgcacagtttttgatgaaagatgcaataaaaccaactgatgacacc	2325
Db	181	TGACAGGTCGTTTGACATTTTGTGAAGAAGATGCAATTAACCAACCAACTGATGCGACACC	240
OY	2326	tggaaaggaaacacctgtgttctgtgaatggggcccttttgtaacattctcaacgcaact	2385
Db	241	TGGAAAGGAACACCTGTGTCTGGCAATGGGGGCCCTTTTGTCAACTTGTCTACGGCAACT	300
OY	2386	cttcagtgltgtgtataaataatgccttcgnaactgtgtgtgtgaagaagatttgaatga	2445
Db	301	CTTCAGTGTGGCTGATTAATAATTGCCCTCGAAACTGGTGTGTAAGAAAGGATTTGTAGTGA	360
OY	2446	ccgaagctgagctttgtgtctgtacacacggaatggagaatctctcaacatcgaagtccgag	2505
Db	361	CCGAAGCTGAGCTTTGTGTGTCTGACATTCGCAATGAGAAATCTTCAACATCAAGTCCGAG	420
OY	2506	cttcagctgtgtgtgcccaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2565
Db	421	CTTCCGGCTGTGGTGCACCAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	480
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Db	601	TCTTTGGGCTTCCCGTTGT	660
OY	2746	tgtgaactgt	2805
Db	661	TTGACTGT	720
OY	2806	actgtgtgcgcttgtgtgaagaagatcgtgtgaactgtgtcgtgtgtgtgtgtgtgtgtgt	2865
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OY	2866	gtataaagaagcgaattccagttccgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2925
Db	781	GTAAGAAAGAACCCATTCCTCAATTCCTGTATATATGTTCAGTGTCCAAATTGTGCACAA	840
OY	2926	ggaacattgtgtcagcgtgtgtctatctgagagcaagaatatgtgaactctctcctgagga	2985
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OY	3166	tgaacacacatgtccagagctgtcccaacccggccctgtttatgtacatagatcttatacgt	3225
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OY	3226	aaacagaacaaatgtaaagctgttcttaagtgtgacaagagctctcaacagagaccgatgag	3285
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OY	3286	acccttgaaagacactccttcgcttccctttgcgcagcttggaagaacctgaattga	3345
OY	3346	aaaatgtcttatggcaatgctgtgagacaatggtgaatataggccaagaattcttcgt	3405
DB	1201	ACTCCTGAACAGACTACTCTTTCCCTTTTTGCGCAGCGTGGAGAACAATGAAATTGTA	1260
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DB	1261	AAAAATGTCTGTTATTCGCAATGCTGGAGACATGCGTAAATATAGGCCMAAATTTCTTCGCT	1320
OY	3406	tcaagataattcttgttacagtgtagatagtgttcttggaagaagaccctccaccaagac	3465
DB	1321	TCAAATATAATTCGTCTTGACAGTAGAGTATAGTITTCGGCAAAAAGACCTCCAGCAAGAC	1380
OY	3466	tgaagaagaactaatlcttctgttctcgtgtgaggtttccattacttcttactgcttaact	3525
DB	1381	TGAAGAAACATAATTTATTTCTGTTTCTGTGGAGTTCCATTTATTTCTACGTCTTACACT	1440
OY	3526	ttaagaatgttattcttattgagggaactaagggtttgagagtgtgaaactaaagttaacctt	3585
DB	1441	TTTGAAGATGTTTATTTTATAGGGACATAAGGGATGTTTAAAGATGTGAACATAAAGTAAACATTT	1500
OY	3586	tccactctcaagtttcttacttctgtcttcttgacagcaataaatacatggatcagaanaacc	3645
DB	1501	TCCACTCTCAATTTTCTTACTTTGTCTTTGAACATGAATAATTAACATGATCTAGAAAAACC	1560
OY	3646	aaaaaaaaaaaaa 3657	
DB	1561	AAAAAAAAAAAAA 1572	
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LOCUS	AC103974	186307 bp DNA linear HTG-27-JAN-2002	
DEFINITION	Homo sapiens chromosome 11 clone RP11-1081L13 map 11, WORKING DRAFT SEQUENCE, 12 ordered pieces.		
ACCESSION	AC103974		
KEYWORDS	AC103974.3 GI:18377266		
SOURCE	HTGS_PHASE2; HTGS_DRAFT; HTGS_FULFLOP.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
REFERENCE	1 (bases 1 to 186307)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
JOURNAL	Homo sapiens chromosome 11, clone RP11-1081L13		
REFERENCE	2 (bases 1 to 186307)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Charazo,B., Choegel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,F., Cooke,P., Deavellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., McArthur,M., McCarty,M., McGowan,P., McKernan,K., McPheters,R., Meldrum,J., Menais,L., Mihova,T., Miengo,V., Murphy,T., Naylor,J., Nguyen,C., Norbud,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,D., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Seaman,S., Severi,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,M.J., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 370 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Jan 27, 2002 this sequence version replaced gi:18308578. All repeats were identified using RepeatMasker:		

74	198.2	5.4	180.3	1	AB006079	AB006079 Sphingomo
75	195.4	5.3	132.1	10	MM006665	U06665 Mus musculus
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79	192	5.3	105.6	1	SM939612	SM939612 Unculture
80	190.6	5.2	203.4	1	AF559462	AF559462 Streptococ
81	184.2	5.0	109.8	1	AF295712	AF295712 Unculture
82	181.8	5.0	105.6	1	AF295704	AF295704 Unculture
83	181.8	5.0	134.1	1	AF295713	AF295713 Unculture
C 84	179	4.9	123.96	9	HSDJ99E18	AF295704 Thermotoma
85	178.6	4.9	105.6	1	AF295713	AL049694 Human DNA
86	177.8	4.9	106.2	1	AF295716	AF295713 Unculture
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C 88	177	4.8	159.478	2	AL359638	AF295719 Unculture
89	176.8	4.8	105.3	1	AL359638	AL359638 Homo sapi
90	176.2	4.8	106.2	1	AF295722	AF295720 Unculture
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92	175.2	4.8	105.3	1	AF295721	AF295706 Eubacteri
93	175.2	4.8	105.6	1	AF295717	AF295720 Unculture
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97	173.8	4.8	106.8	1	AF295707	AF270090 Staphyloc
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99	171.6	4.7	96.7	8	AB026196	AF295707 Ruminococ
100	170.6	4.7	96.7	8	AB026196	AB026196 Unculture
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C 102	169.8	4.6	301550	1	AF295702	AF295702 Clostridi
C 103	169.8	4.6	342600	1	AP001334	AP003134 Staphyloc
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106	166.8	4.6	105.6	2	AL359638	AL359638 Homo sapi
107	166.4	4.6	105.6	1	AF295705	AF295705 Clostridi
108	162.8	4.5	109.8	1	AF459463	AF459463 Unculture
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C 111	161.2	4.4	105.6	1	AF295715	AF295701 Acetobact
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C 123	139	3.8	105.6	1	AP295714	AF295714 Homo sapi
C 124	138	3.8	303040	1	AP000991	AF295714 Unculture
C 125	134.4	3.7	6272	1	ZMNDRAP	AP000991 Thermopla
C 126	129.8	3.5	371.3	6	AX145058	X84019 z. mobilis g
C 127	129.8	3.5	371.3	6	AX145058	AF269740 Staphyloc
128	127	3.5	288	6	AX307928	AX145058 Sequence
C 129	125	3.4	66291	2	AC1039328	AX307796 Sequence

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VERSION      ALL117452.1   GI:5911902
KEYWORDS
SOURCE
ORGANISM     human.
              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 3164)
AUTHORS      Koehner, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE        Direct Submission
JOURNAL       Submitted (15-SEP-1999) MIPS, Am Klopferspitz 18a, D-82152
              Martinsried, GERMANY
COMMENT      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
              Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
              Sequenced by BMFZ (Biomedical Research Center at the Charite,
              Berlin/Germany) within the cDNA sequencing consortium of the Germ
              Genome Project.
              This clone (DKFP586G1517) is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
              information about the clone and the sequencing project is availab
              at http://www.mips.biochem.mpg.de/proj/cdna/.

FEATURES
source
location/Qualifiers
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                polyA_site
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ORIGIN
Query Match      85.9%; Score 3142.8; DB 9; Length 3164;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3157; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

496 gaagcccgccgcccgaacgcggcgaggctcatcgtaagaagaatcattcaga 555
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Matches 3157; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

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Db 61 ATTCAAAGAAGTTCTAGATTATTATTCGAAGAAAAAACCCGCCCTTAAGCCG GTTCTT

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Db	181	AGGCTGGTCTGAAACATCACTCACTTTTGGCTCCCTCCAGATGACGTGAAGCCGACATT	240
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Db	241	TAGATGAATCTTAAAGATCAATGAATACGATACGAGATCAATGGCTTGCCTTCAGATCT	300
QY	796	ctgagaacttgcttagcaaaaagctcctcaatgccttgaaaccaagaaaagatgtagatg	855
Db	301	CTGGAAACTGTGTTAGCAACCAAACTCTCAATGCTTGAAACAGAAAAGATGTGATG	360
QY	856	gagtaaacagacataaacctctgggagagcttggctgagagggaatgcccataatgtttgt	915
Db	361	GAGTAACAGACATTAACCTGGGGAAGCTGGGCGACGAGGGATGCCCAATGATTTGTGTT	420
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Db	538	TCCAGAGAAAAGGGTCCATGCAATGACATTCAGATGGAACACGCCAGCTTTAAAGCA	597
QY	1096	agcttcaagagagctgacatctggctcctaagctcaactaaagccagaagagatccocctta	1155
Db	598	AGCTTCAAGAGAGCTGACATTTGGTGGTCCTAGGCTCACTTAACCCAGAAAGATTTCCCTTA	657
QY	1156	cttgatataaacccaggaactactgttcccaactgtcccaagactcctgfcagaagag	1215
Db	658	CTTGATATCAACCAAGAACTACTGTTCTCAATGCTCCATGACTCTCTGTACAGGAAGG	717
QY	1216	ttgggttggtctcccaagaatatacttttggctgacatcttgaagaaatgtagtgaatc	1275
Db	718	TTGGGTGGTGGCTCCAAAGATATCAATTTGGTGGGACTCATTGAGGAAATGATGTGATTC	777
QY	1276	tccctgtgcagctctcggaaatcagaacatgtagtaagtggaaggaatggcttctgtg	1335
Db	778	TCCCTGTGCACCTCTGGGAATTCGAACATGCTAGTAGTGAAGAGATGGCTTGGTG	837
QY	1336	aacagacagacagcgctggtagacttcaactcgtctgaacttaagcctctcccccgtgc	1395
Db	838	AACAGACAGACAGGGGGTGAAGACTCACTGCTTGAACCTTAGCCCTCTCCCTGTGAC	897
QY	1396	caagtgaacattgagattccaagagagacaactccaaaagctgtgtagtctccttgcgaag	1455
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QY	1456	agattgagattgcttcagaatgaatgaactatagcaaaagcaaaagcaaaagtaagtt	1515
Db	958	AGATTGGAATGCTTGCAGATGGAATTTGAATCTATGCGCAAAAAGCAAAAGCAAAATGACGTT	1017
QY	1516	tgctcgtctagaaaaggttaaagatcaagcagaatgaataacgtcttaagtctgtggga	1575
Db	1018	TGCTCGTCTAGAAAAGTTAAAGATTAAGGATCAAGCATGTGAAAATACGCTTAGTGTCTGGGA	1077
QY	1576	tccaccaccaccctcttggaaagaggaagacagtaacatccggtctgtgcaggtcc	1635
Db	1078	TCCACCCACACCTCTTTGGAGAAAGGAGACGCAATTCACATCGGGCTTGTGCAGGCTC	1137
QY	1636	tgcgcgcacacactgaaatgtcaacttccttgcctgtcttgaagcagcttcccaagacga	1695
Db	1138	TGAACCGACACCTGAATGTCAATCCCTTTCCTGCTTGAAGGCGAGCCTTCCCAAGGACGA	1197

QY	1696	cgcttgtagtgaagaagagagccgacgagtgtagtatatcccaaggtcatcccaatggag	1755
Db	1198	CGTTTGAGTAAAGAGAGAGACCAGGAGTGGTGAATATGCCAGGTCAATCCCATGAGAG	1257
QY	1756	agttcaaccttacttgaactgagagacatccagccatccacgcgtgcgaataactgtcg	1815
Db	1258	AGTTCAACCTTCACCTTGACTGAGACATCCACGCCATCAACCGCTGCCAATAACTTGCTGG	1317
QY	1816	ctgcgcgcattcgaaacagagattcttataaacaacgaaagaagaagtagtata	1875
Db	1318	CTGCCGCATCGACACGAGGATTTTATGTAAGAACACGCAAAAGATTAAGCTCTTATA	1377
QY	1876	atcgcgtgttcctttagtgaatggttgcagagaatttccaagaattcagactgtccg	1935
Db	1378	ATCGGCTGTGTTCTTTATGTAATGGTGTGAGAGATTTTCAGAAATTCACCTGTCTGGC	1437
QY	1936	taaaaaaacctgggaataataataagactatccgagcacactgacaagaaggaagtagta	1995
Db	1438	TAAAAAAACCTGGGAATTAATTAAGACTGTATCGACACATCGACAGAAAGAAAGTAGATA	1497
QY	1996	aatttgcgcgtctcgacatcgaccacttaccatcacagctggcagagagtagtatgataa	2055
Db	1498	AATTTGCCGCTCGACATCGAACCCATCTACATCACGTGGCAGAGAGTATGGATACAA	1557
QY	2056	atgaccgatttctaaagaaaaataacatctggcgcagggaacaagaagaagggcattacc	2115
Db	1558	ATGACCGAATTTCTACGAAAAATACCAATCGGGCAGGAAACACAGAAAGGCCATTACC	1617
QY	2116	ggcagcgagctttagacatcgcaatgycgcagcagatcatatggcgtgtcgtcccttaccg	2175
Db	1618	GCGAGCGCAGTTTACATCGAGTGGCGACAGATCATGGCGGTGCTGGCCCTGACGG	1677
QY	2176	acagcctcgacagacatgaaggaacgcgcttgggaagatggtgtgtgtccagtgtgacaaaagc	2235
Db	1678	ACAGCCTCCCAACATGAAGGCAACGCTGGGAAGAGATGTGTGGCCAGTGACAAAAAGCG	1737
QY	2236	ggagagccttgcacagatatgatttgggggtggacaggtgtcttgcagatttgaatgaag	2295
Db	1738	GCGAGCCTGTGACAGCATATGATTTTGGGGGTGACAGGTGCTTACAGTTTATGTAAG	1797
QY	2296	atgcaataaacaacaaactgtatgcagacccttggaaaggacaactgtgttcgttgcatacg	2355
Db	1798	ATGCATTAATAAACCAACCTGATGCGACGCCCTGGAAAGGACACCTGTGTCGTGATCGG	1857
QY	2356	ggccttcttctaacatgttctacgcgcaactcttcaagtgttgcgtataaaatttgcctga	2415
Db	1858	GCCCTTTGTATCACTTGTCTCACGGCACTCTTCAGTGTGGCTGATTAATAATTGCTCTGA	1917
QY	2416	aactgtgtgtgaagaagatttgaatgtgacccgaagctgtgccttgtgtctgacatcgaa	2475
Db	1918	AACGTGTGGTGAAGAAGATTTGTATGTAACCGAAGCTGGCTTGTGCTGACATCGAA	1977
QY	2476	tggagaatttctcaacatcaatgctgcgcgcgtcttcgcgttgttgcgcaagttgttgt	2535
Db	1978	TGGAGAAATTCCTCAACATCAATAGTGTCCGAGCTTCGGCTGTGATGCCAAACGTGTGTGT	2037
QY	2536	taatggaacgctgtgcagctctgaagaatgcatgagagcggtggcgaagtgtaaacgctgtgt	2595
Db	2038	TAGTGGCAACGGTGCGAGCTGTGAAGATGCATGAGAGCGGGCCAGGTATACGGCTGTGTG	2097
QY	2596	tctcctctaaagaagaatatacagagagaaacatccagctgtgtgtgcacagcgtgtctta	2655
Db	2098	TTCTCTTTAAGAAAGATATACAGAGAGAAACATCAAGTGTGTGCAACGGCTGTCTTA	2157
QY	2656	accctcagaagaatccagatcacccacgctcttggagtttccgctgtgtgtgtcctga	2715
Db	2158	ACCTCCAGAAACCAATTCATATCAATCAAGTCTTTGGGGTTTCCCGTGTGTGGGTCTCGA	2217
QY	2716	atgtcttcaagaccgacaccgcgtctgaagattgaactgtgtgtgaagcttgcacaaagcg	2775
Db	2218	ATGCTTCAAGACCGAACCCCGGCTGAGATTAATCTTGCTGTGAGCTTGCACAAAGCGGG	2277
QY	2776	ctgagtgcctttagtgaagtcctccctgtatcatcacgtgtcgtgttgtgtaaaagaatcgtgtg	2835

Mon Aug 19 15:11:21 2002

RESULT 2
 BC017477
 LOCUS
 DEFINITION BC017477
 Homo

accession VERSION keywords SOURCE ORGANISM
 formyltetrahydrofolate dependent), methenyltetrahydrofolate dehydrogenase
 mRNA, complete cds. 2749 bp mRNA linear PRI 21-NOV-2001
 BC017477
 BC017477.1 GI:17028347
 MGC.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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QY 1044 aaatggtccacagcaatgagcatccagttggaataacacgccca
 Db 1118 AAAGGCTTCACGCAAAAGACCATGAGTGGAATAACAGCCCA
 QY 1104 gaggctgacatctgggtccctaaagctaacccgaagccagaagat
 Db 178 GAGGCTGCATTGGTGGCTCAAGGCTCACTAAGCCAGAGAAAGAC
 QY 1164 caaccaggaactactgtgtccaactgtccacgaagctctctg
 Db 238 CAAACAGAGAACACACTGTCTCAACAGCTCTCCATGACTCTCG
 QY 1224 ggtcttccaaagaatcatcttggtagaactattggaagaat
 Db 298 GGGCTTCCAAAGATTAACATTTGTGTGATCCATTTGAGGAAGAT
 QY 1284 gcaactctggaattgaagaacttgcagttcagttggaagaaga
 Db 358 GCAGCTCTGCGAATTAGAAATGCTCAGTGTGGAAGGAGA
 QY 1344 cacaggcggltggaacttcatctgcttmaacttcaagctctc
 Db 418 CAAAGCGGTGGAGACTTCACTGGCTGAAATTCAGGCTCTC